

PALM INTRANET

Day : Monday
Date: 1/14/2008

Time: 20:29:26

Inventor Name Search

10/539,178

Enter the **first few letters** of the Inventor's Last Name.
Additionally, enter the **first few letters** of the Inventor's First name.

Last Name**First Name**

Flanigan

Kevin

Search

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PALM INTRANETDay : Monday
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#1 Search White S AND DMD	17:15:12	<u>7</u>

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SCORE Search Results Details for Application 10539178 and Search Result 20080109_150537_us-10-539-178-1.rng.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:09:18 ; Search time 290 Seconds
(without alignments)
745.652 Million cell updates/sec

Title: US-10-539-178-1
Perfect score: 20
Sequence: 1 aattggcaccagagaaatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200711:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2004c:*
15: geneseqn2004d:*

16: geneseqn2005a:*
 17: geneseqn2005b:*
 18: geneseqn2005c:*
 19: geneseqn2006a:*
 20: geneseqn2006b:*
 21: geneseqn2006c:*
 22: geneseqn2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	20	100.0	20	13	ADQ13606			Adq13606 DMD regio
c	2	18.4	92.0	886	14	AGE30203			Age30203 Human sin
c	3	18.4	92.0	85869	15	AFI70361			Afi70361 Human gen
c	4	18.4	92.0	85878	15	AFI74665			Afi74665 Human gen
	5	17.4	87.0	101365	16	AEP71437			Aep71437 Alzheimer
	6	17.4	87.0	101365	21	AGA38905			Aga38905 Alzheimer
	7	17.4	87.0	172781	17	AED89385			Aed89385 Human bre
c	8	17	85.0	1189	14	AEX05694			Aex05694 Bovine sp
c	9	17	85.0	1189	14	AEW40747			Aew40747 Bovine sp
	10	16.8	84.0	201	14	AEX54475			Aex54475 Human rhe
	11	16.8	84.0	201	14	AEX54472			Aex54472 Human rhe
c	12	16.8	84.0	544	4	AAK10343			Aak10343 Human bra
c	13	16.8	84.0	544	4	ABA62026			Aba62026 Human foe
c	14	16.8	84.0	544	4	AAI41964			Aai41964 Probe #10
c	15	16.8	84.0	544	4	ABS35926			Abs35926 Human liv
c	16	16.8	84.0	544	4	ABA29497			Aba29497 Probe #79
c	17	16.8	84.0	544	4	AAK36244			Aak36244 Human bon
c	18	16.8	84.0	544	4	AAI17257			Aai17257 Probe #71
c	19	16.8	84.0	544	6	ABS10337			Abs10337 Human gen
c	20	16.8	84.0	545	14	AGE91644			Age91644 Human sin
c	21	16.8	84.0	545	14	AGE84880			Age84880 Human sin
c	22	16.8	84.0	546	14	AGE32574			Age32574 Human sin
	23	16.8	84.0	551	14	AGE32930			Age32930 Human sin
	24	16.8	84.0	551	15	AGE32931			Age32931 Human sin
	25	16.8	84.0	553	14	AGE32573			Age32573 Human sin
c	26	16.8	84.0	569	14	AGH48999			Agh48999 Human sin
	27	16.8	84.0	584	14	AGG06871			Agg06871 Human sin
	28	16.8	84.0	658	14	AGH02802			Agh02802 Human sin
	29	16.8	84.0	658	15	AGH02801			Agh02801 Human sin
	30	16.8	84.0	1334	14	AGG32845			Agg32845 Human sin
	31	16.8	84.0	1370	1	AAN82410			Aan82410 Plasmid p
	32	16.8	84.0	1370	10	ADB52335			Adb52335 Primary r
	33	16.8	84.0	1626	22	AFQ96317			Afq96317 Rat type
	34	16.8	84.0	2266	8	ABT41702			Abt41702 Toxicity
	35	16.8	84.0	2266	10	ADB52339			Adb52339 Primary r
	36	16.8	84.0	2266	13	ADV40787			Adv40787 Rat cardi
c	37	16.8	84.0	3218	5	ABL06670			Abl06670 Drosophil
c	38	16.8	84.0	3218	17	AFB87203			Afb87203 Fruit fly
	39	16.8	84.0	16922	18	AGD78652			Agd78652 Human gen
	40	16.8	84.0	16923	18	AGD78689			Agd78689 Human gen
	41	16.8	84.0	30057	11	ACN44664			Acn44664 Mouse gen
c	42	16.8	84.0	50000	9	ADC56844			Adc56844 Human ATP
c	43	16.8	84.0	56423	8	ADC85728			Adc85728 Human GPC
c	44	16.8	84.0	73063	13	ADQ97727			Adq97727 Human can

SCORE Search Results Details for Application 10539178 and Search Result 20080109_150537_us-10-539-178-187.rng.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:09:18 ; Search time 319 Seconds
(without alignments)
745.652 Million cell updates/sec

Title: US-10-539-178-187
Perfect score: 22
Sequence: 1 cactgtgctattctggtttgga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200711:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
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15: geneseqn2004d:*

16: geneseqn2005a:*
 17: geneseqn2005b:*
 18: geneseqn2005c:*
 19: geneseqn2006a:*
 20: geneseqn2006b:*
 21: geneseqn2006c:*
 22: geneseqn2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID			
1	22	100.0	22	13	ADQ13792			Adq13792 DMD regio
c 2	17.8	80.9	1510	8	ADK59908			Adk59908 Plant DNA
c 3	17.8	80.9	1510	8	ADK56233			Adk56233 Plant DNA
4	17.8	80.9	2805	15	AFO56327			Afo56327 Glycine m
5	17.4	79.1	601	15	AFJ20862			Afj20862 Human DNA
c 6	17.4	79.1	163662	15	AFI70889			Afi70889 Human gen
c 7	17.4	79.1	163664	15	AFI71890			Afi71890 Human gen
8	17.2	78.2	601	15	AFJ12221			Afj12221 Human DNA
c 9	17.2	78.2	700	4	AAH93101			Aah93101 Human inf
c 10	17.2	78.2	859	14	AGE58571			Age58571 Human sin
11	17.2	78.2	1085	14	AEW90937			Aew90937 Bovine sp
12	17.2	78.2	1085	14	AEW25991			Aew25991 Bovine sp
c 13	17.2	78.2	2006	14	AEW79027			Aew79027 Bovine sp
c 14	17.2	78.2	2006	14	AEW14081			Aew14081 Bovine sp
15	17.2	78.2	2335	9	ADB62550			Adb62550 Human cDN
16	17.2	78.2	2885	12	ADX50184			Adx50184 Plant ful
17	17.2	78.2	3056	19	AFC58776			Afc58776 Maize cDN
18	17.2	78.2	3234	20	AFK73017			Afk73017 Polymorph
19	17.2	78.2	3941	14	AEW75798			Aew75798 Bovine sp
20	17.2	78.2	3941	14	AEW10852			Aew10852 Bovine sp
21	17.2	78.2	10118	22	AFB68168			Afb68168 Mouse kin
22	17.2	78.2	30072	11	ACN44152			Acn44152 Mouse gen
23	17.2	78.2	75176	15	AFI71644			Afi71644 Human gen
24	17.2	78.2	83784	16	AEP71425			Aep71425 Alzheimer
25	17.2	78.2	83784	20	AGA38893			Aga38893 Alzheimer
26	17.2	78.2	110000	11	ACN44934_2			Continuation (3 of
c 27	17.2	78.2	110000	13	ABD32780_3			Continuation (4 of
28	17.2	78.2	110000	15	AFI71517_1			Continuation (2 of
29	17.2	78.2	110000	16	ADZ46976_4			Continuation (5 of
c 30	17.2	78.2	187136	15	AFI75575			Afi75575 Human gen
c 31	17.2	78.2	294575	16	AEA61217			Aea61217 Human STK
c 32	17.2	78.2	313287	13	ABD33100			Abd33100 Human can
c 33	17.2	78.2	313287	19	AEJ13040			Aej13040 Cancer-as
c 34	17	77.3	2865	19	AEH40248			Aeh40248 Cryptospo
35	16.8	76.4	282	3	AAA44291			Aaa44291 Human sec
c 36	16.8	76.4	492	15	AGG56864			Agg56864 Human sin
c 37	16.8	76.4	492	15	AGG56863			Agg56863 Human sin
c 38	16.8	76.4	501	22	AER72552			Aer72552 Bovine tr
39	16.8	76.4	549	8	ACF56843			Acf56843 Rice leaf
40	16.8	76.4	652	14	AGF26732			Agf26732 Human sin
41	16.8	76.4	887	14	AGE34784			Age34784 Human sin
42	16.8	76.4	887	14	AGE34785			Age34785 Human sin
43	16.8	76.4	887	15	AGE34786			Age34786 Human sin
c 44	16.8	76.4	996	14	AEW65527			Aew65527 Bovine sp

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Title: US-10-539-178-188
Perfect score: 24
Sequence: 1 tttatgcttctttgcaaactactg 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200711:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2004c:*
15: geneseqn2004d:*

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 17: geneseqn2005b:*
 18: geneseqn2005c:*
 19: geneseqn2006a:*
 20: geneseqn2006b:*
 21: geneseqn2006c:*
 22: geneseqn2007:*

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SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	13	ADQ13793	Adq13793 DMD regio
	2	22.4	93.3	601	15	AFK48071	Afk48071 Human DNA
	3	22.4	93.3	197131	15	AFI71019	Afi71019 Human gen
	4	22.4	93.3	197132	15	AFI75514	Afi75514 Human gen
	5	19.2	80.0	600	17	AFI41012	Afi41012 Chicken s
	6	19.2	80.0	600	17	AFI41010	Afi41010 Chicken s
	7	19.2	80.0	600	17	AFI41011	Afi41011 Chicken s
	8	19.2	80.0	1493	19	AEL26508	Ael26508 Human cDN
	9	19.2	80.0	2966	19	AEJ45416	Aej45416 Human G p
	10	19.2	80.0	2970	16	ADY17168	Ady17168 DNA encod
	11	18.8	78.3	514	10	ADE81377	Ade81377 Arabidops
c	12	18.8	78.3	539	6	ABN62278	Abn62278 Human can
c	13	18.8	78.3	539	16	ACL58171	Acl58171 Human col
c	14	18.8	78.3	539	17	AGD43119	Agd43119 Human pol
	15	18.8	78.3	3453	20	AFY34287	Afy34287 Saccharom
	16	18.8	78.3	3453	21	AGB18665	Agb18665 Saccharom
c	17	18.4	76.7	912	8	ACF72332	Acf72332 Staphyloc
c	18	18.4	76.7	1578	2	AAV74527	Aav74527 Staphyloc
	19	18.2	75.8	57	6	ABN84050	Abn84050 Glutamate
	20	18.2	75.8	99	6	ABN84035	Abn84035 Single ch
c	21	18.2	75.8	570	12	ADL87078	Adl87078 DNA up-re
c	22	18.2	75.8	570	12	ADL87077	Adl87077 DNA up-re
c	23	18.2	75.8	600	14	AEW61711	Aew61711 Bovine sp
c	24	18.2	75.8	600	14	AEV96764	Aev96764 Bovine sp
c	25	18.2	75.8	601	15	AFJ99780	Afj99780 Human DNA
	26	18.2	75.8	633	22	AEM76588	Aem76588 Soybean (
c	27	18.2	75.8	675	13	AET08474	Aet08474 C. albica
c	28	18.2	75.8	931	14	AEX00449	Aex00449 Bovine sp
c	29	18.2	75.8	931	14	AEW35502	Aew35502 Bovine sp
c	30	18.2	75.8	1355	14	AEW67443	Aew67443 Bovine sp
c	31	18.2	75.8	1355	14	AEW02497	Aew02497 Bovine sp
	32	18.2	75.8	1371	5	AAS76855	Aas76855 DNA encod
c	33	18.2	75.8	8450	13	ADR84479	Adr84479 Aspergill
	34	18.2	75.8	236964	15	AFI74097	Afi74097 Human gen
	35	17.8	74.2	200	15	AFP47448	Afp47448 Glycine m
	36	17.8	74.2	384	10	ADF57738	Adf57738 Human pol
c	37	17.8	74.2	586	13	ACN45257	Acn45257 Cotton pr
c	38	17.8	74.2	600	18	AFU84500	Afu84500 Human pro
	39	17.8	74.2	803	14	AGG01762	Agg01762 Human sin
	40	17.8	74.2	803	14	AGG01763	Agg01763 Human sin
	41	17.8	74.2	2280	13	ADQ22219	Adq22219 Human sof
	42	17.8	74.2	2646	5	ABL07099	Abl07099 Drosophil
	43	17.8	74.2	2646	17	AFB87846	Afb87846 Fruit fly
	44	17.8	74.2	2655	10	ADM02480	Adm02480 Human cDN

SCORE Search Results Details for Application 10539178 and Search Result 20080109_150537_us-10-539-178-2.rng.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:09:18 ; Search time 347 Seconds
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745.652 Million cell updates/sec

Title: US-10-539-178-2
Perfect score: 24
Sequence: 1 tcatgtgttttagttctatcgcaa 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200711:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2004c:*
15: geneseqn2004d:*

16: geneseqn2005a:*
 17: geneseqn2005b:*
 18: geneseqn2005c:*
 19: geneseqn2006a:*
 20: geneseqn2006b:*
 21: geneseqn2006c:*
 22: geneseqn2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		DB	ID	Description
			Match	Length			
	1	24	100.0	24	13	ADQ13607	Adq13607 DMD regio
c	2	24	100.0	132	2	AAQ66654	Aaq66654 Fragment
c	3	18.2	75.8	1039	15	AFO98879	Afo98879 Glycine m
c	4	18.2	75.8	130130	19	AEM23543	Aem23543 Human TAT
c	5	18.2	75.8	163022	15	AFI74859	Afi74859 Human gen
	6	18.2	75.8	221600	16	ADX80720	Adx80720 Human neu
	7	17.6	73.3	399	10	ACH48970	Ach48970 Human leu
	8	17.6	73.3	507	7	ADW41630	Adw41630 cDNA elev
	9	17.6	73.3	507	7	ADS72776	Ads72776 Human kid
c	10	17.6	73.3	549	2	AAT83808	Aat83808 DNA encod
	11	17.6	73.3	601	15	AFK53912	Afk53912 Human DNA
	12	17.6	73.3	601	15	AFI97130	Afi97130 Human DNA
	13	17.6	73.3	645	6	AAS61746	Aas61746 Lung smal
	14	17.6	73.3	645	8	ADD66935	Add66935 Human lun
	15	17.6	73.3	645	10	ADE88189	Ade88189 Human lun
	16	17.6	73.3	927	14	AEW77568	Aew77568 Bovine sp
	17	17.6	73.3	927	14	AEW12622	Aew12622 Bovine sp
	18	17.6	73.3	946	5	AAI97773	Aai97773 Human neu
	19	17.6	73.3	1400	18	AFU82077	Afu82077 Human pro
c	20	17.6	73.3	1597	13	ADO60399	Ado60399 (R)-hydro
c	21	17.6	73.3	1609	13	ADO60400	Ado60400 (R)-hydro
c	22	17.6	73.3	1632	6	AAF88779	Aaf88779 P. amygda
c	23	17.6	73.3	1632	16	AEC39603	Aec39603 Almond hy
c	24	17.6	73.3	1680	19	AEH91897	Aeh91897 Prunus du
c	25	17.6	73.3	1680	19	AEH91900	Aeh91900 Prunus du
	26	17.6	73.3	2000	8	ACL36093	Ac136093 Rice stre
c	27	17.6	73.3	2162	6	AAF88778	Aaf88778 Almond md
c	28	17.6	73.3	2162	16	AEC39601	Aec39601 Almond hy
	29	17.6	73.3	2241	8	ADG10551	Adg10551 Human STA
	30	17.6	73.3	2494	4	AAS31100	Aas31100 Human dia
	31	17.6	73.3	2690	4	AAH14245	Aah14245 Human cDN
	32	17.6	73.3	2815	2	AAZ77532	Aaz77532 Human ova
	33	17.6	73.3	3056	13	ADO35558	Ado35558 Novel mou
	34	17.6	73.3	3172	12	ADL12671	Adl12671 Human ste
	35	17.6	73.3	3791	10	ADG77060	Adg77060 Human nuc
	36	17.6	73.3	3803	8	ADG10859	Adg10859 Human STA
	37	17.6	73.3	3803	17	AED18337	Aed18337 Fibrotic
	38	17.6	73.3	3815	8	ADG10553	Adg10553 Human STA
	39	17.6	73.3	3817	15	AFI63896	Afi63896 Human cDN
	40	17.6	73.3	3835	15	AFI59411	Afi59411 Human cDN
	41	17.6	73.3	3835	17	AED14299	Aed14299 Human cum
	42	17.6	73.3	3835	17	AFU76842	Afu76842 Human pro
	43	17.6	73.3	3839	4	AAF32759	Aaf32759 Human sec
	44	17.6	73.3	3839	8	ABZ73486	Abz73486 Secreted

SCORE Search Results Details for Application : Result 20080109_150539_us-10-539

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This page gives you Search Results detail for the Application 10539178 and Search Result 20080109

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:12:07 ; Search time 1145 Seconds
(without alignments)
1429.452 Million cell updates/sec

Title: US-10-539-178-1
Perfect score: 20
Sequence: 1 aattggcaccagagaaatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_in:*
13: gb_om:*
14: gb_ba:*
15: gb_htg1:*
16: gb_htg2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	20	100.0	1387	5	HUMDMDPR	M32058 Human Duche
2	20	100.0	11747	5	AF276053S1	AF276053 Homo sapi
c 3	20	100.0	133889	5	AL031643	AL031643 Human DNA
c 4	20	100.0	185393	5	CR956355	CR956355 Pan trogl
5	19	95.0	913	7	BV473540	BV473540 G591P6253
c 6	19	95.0	42246	5	Z82253	Z82253 Human DNA s
7	19	95.0	178717	5	AC194803	AC194803 Pan trogl
8	19	95.0	182897	16	AL158202	AL158202 Homo sapi
c 9	18.4	92.0	754	7	BV499640	BV499640 S222P6607
c 10	18.4	92.0	1545	12	AK223668	AK223668 Toxoplasm
11	18.4	92.0	52720	15	AC107997	AC107997 Homo sapi
12	18.4	92.0	62019	5	AC105239	AC105239 Homo sapi
c 13	18.4	92.0	83767	5	AC114307	AC114307 Homo sapi
14	18.4	92.0	110000	12	AM055943_18	Continuation (19 o
c 15	18.4	92.0	117100	5	AC137741	AC137741 Homo sapi
c 16	18.4	92.0	125535	5	AC073385	AC073385 Homo sapi
17	18.4	92.0	129361	5	AL603789	AL603789 Human DNA
18	18.4	92.0	134124	5	AL160266	AL160266 Human DNA
c 19	18.4	92.0	134580	15	AC025359	AC025359 Homo sapi
20	18.4	92.0	138740	5	AC008063	AC008063 Homo sapi
21	18.4	92.0	139409	5	AC069181	AC069181 Homo sapi
c 22	18.4	92.0	142557	5	AL356499	AL356499 Human DNA
23	18.4	92.0	144200	15	AC022638	AC022638 Homo sapi
c 24	18.4	92.0	152304	15	AC023032	AC023032 Homo sapi
25	18.4	92.0	158699	5	AP006183	AP006183 Homo sapi
26	18.4	92.0	158852	15	AC023023	AC023023 Homo sapi
c 27	18.4	92.0	162063	16	AC156381	AC156381 Rhinoloph
c 28	18.4	92.0	166215	5	CT826194	CT826194 Pan trogl
c 29	18.4	92.0	167876	16	AC156384	AC156384 Rhinoloph
30	18.4	92.0	171131	5	AC191957	AC191957 Rhesus Ma
31	18.4	92.0	173065	6	AC116740	AC116740 Mus muscu
c 32	18.4	92.0	174926	5	CT998538	CT998538 Pan trogl
33	18.4	92.0	176032	5	AC194673	AC194673 Pan trogl
34	18.4	92.0	183903	15	AC020684	AC020684 Homo sapi
35	18.4	92.0	184470	5	AC187130	AC187130 Callithri
36	18.4	92.0	185859	15	AC068026	AC068026 Homo sapi
c 37	18.4	92.0	188873	5	AC193035	AC193035 Pan trogl
38	18.4	92.0	205673	6	AC126688	AC126688 Mus muscu
39	18.4	92.0	212598	6	AC158898	AC158898 Mus muscu
c 40	18.4	92.0	223953	15	AC122973	AC122973 Rattus no
c 41	18.4	92.0	226284	6	AC099609	AC099609 Mus muscu
42	18.4	92.0	227181	15	AC121010	AC121010 Rattus no
43	18.4	92.0	237143	15	AC073769	AC073769 Mus muscu
44	18.4	92.0	237450	15	AC095092	AC095092 Rattus no
45	18.4	92.0	240486	15	AC095305	AC095305 Rattus no

ALIGNMENTS

RESULT 1

HUMDMDPR

LOCUS HUMDMDPR 1387 bp DNA linear PRI 07-NOV-1994

DEFINITION Human Duchenne muscular dystrophy gene, exon 1.

SCORE Search Results Details for Application 10539178 and Search Result 20080109_150539_us-10-539-178-187.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10539178 and Search Result 20080109_150539_us-10-539-178-187.rge.

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:12:07 ; Search time 1260 Seconds
(without alignments)
1429.452 Million cell updates/sec

Title: US-10-539-178-187
Perfect score: 22
Sequence: 1 cactgtgctattctggtttgga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_in:*
13: gb_om:*
14: gb_ba:*
15: gb_htgl:*

16: gb_htg2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	22	100.0	616	5	AF213401	AF213401 Homo sapi
	2	22	100.0	1387	5	HUMDM DPR	M32058 Human Duche
	3	22	100.0	11747	5	AF276053S1	AF276053 Homo sapi
c	4	22	100.0	133889	5	AL031643	AL031643 Human DNA
c	5	22	100.0	185393	5	CR956355	CR956355 Pan trogl
	6	20.4	92.7	470	6	MUSDMD	M86232 Mouse dystro
	7	20.4	92.7	927	6	MUSDP	D83217 Mus musculu
	8	20.4	92.7	110000	16	BX294176_0	BX294176 Mus muscu
c	9	20.4	92.7	158789	16	AC154120	AC154120 Mus muscu
	10	20.4	92.7	237321	6	AL731776	AL731776 Mouse DNA
	11	19.4	88.2	147851	16	AC170035	AC170035 Muntiacus
	12	19.4	88.2	156728	16	AC170044	AC170044 Muntiacus
	13	19.4	88.2	173410	15	AC115330	AC115330 Rattus no
	14	19.4	88.2	188533	16	AC168950	AC168950 Muntiacus
c	15	19.4	88.2	220171	15	AC113111	AC113111 Mus muscu
c	16	19.4	88.2	225302	6	AC109205	AC109205 Mus muscu
	17	19.4	88.2	227631	15	AC108564	AC108564 Rattus no
	18	19	86.4	209920	15	AC073682	AC073682 Mus muscu
	19	18.8	85.5	468	6	RATDMD	M86233 Rat dystrop
c	20	18.8	85.5	107109	5	AL118522	AL118522 Human DNA
	21	18.8	85.5	110000	14	CP000688_08	Continuation (9 of
	22	18.8	85.5	110000	14	AJ965256_07	Continuation (8 of
c	23	18.8	85.5	150005	5	AL450344	AL450344 Human DNA
c	24	18.8	85.5	173568	16	AC190427	AC190427 Cavia por
c	25	18.8	85.5	178481	16	CU464155	CU464155 Sus scrof
	26	18.8	85.5	187152	16	AC162007	AC162007 Bos tauru
c	27	18.8	85.5	190535	16	AC153735	AC153735 Chloroce
c	28	18.8	85.5	197337	16	CU466241	CU466241 Sus scrof
c	29	18.8	85.5	208088	16	AC169143	AC169143 Callicebu
c	30	18.8	85.5	229264	15	AC131219	AC131219 Rattus no
c	31	18.8	85.5	231767	15	AC094531	AC094531 Rattus no
	32	18.8	85.5	234588	15	AC103209	AC103209 Rattus no
	33	18.8	85.5	235718	16	AC162337	AC162337 Bos tauru
	34	18.8	85.5	236874	15	AC115267	AC115267 Rattus no
	35	18.4	83.6	2902	4	X83077	X83077 Z.mays Fer2
	36	18.4	83.6	40383	6	AC167120	AC167120 Mus muscu
	37	18.4	83.6	43020	6	AC169082	AC169082 Mus muscu
	38	18.4	83.6	52568	5	AC093702	AC093702 Homo sapi
c	39	18.4	83.6	178218	15	AC016841	AC016841 Homo sapi
	40	18.4	83.6	195003	6	AL731871	AL731871 Mouse DNA
	41	18.4	83.6	211442	15	AC109502	AC109502 Mus muscu
c	42	18	81.8	163648	15	AC142370	AC142370 Rattus no
	43	18	81.8	198211	15	AC073756	AC073756 Mus muscu
	44	18	81.8	224227	15	AC106509	AC106509 Rattus no
	45	18	81.8	256059	15	AC098893	AC098893 Rattus no

ALIGNMENTS

SCORE Search Results Details for Application 10 Result 20080109_150539_us-10-539-1

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This page gives you Search Results detail for the Application 10539178 and Search Result 20080109

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:12:07 ; Search time 1374 Seconds
(without alignments)
1429.452 Million cell updates/sec

Title: US-10-539-178-188
Perfect score: 24
Sequence: 1 tttatgcttctttgcaaactactg 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_in:*
13: gb_om:*
14: gb_ba:*
15: gb_htg1:*
16: gb_htg2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
			Match	Length	Score	Length			
c	1	24	100.0	1387	5	HUMDM DPR			M32058 Human Duche
c	2	24	100.0	11747	5	AF276053S1			AF276053 Homo sapi
	3	24	100.0	133889	5	AL031643			AL031643 Human DNA
	4	24	100.0	185393	5	CR956355			CR956355 Pan trogl
	5	22.4	93.3	211662	5	AL391825			AL391825 Human DNA
c	6	20.8	86.7	160282	16	AC167490			AC167490 Bos tauru
c	7	20.4	85.0	77948	15	AC018982			AC018982 Homo sapi
	8	20.4	85.0	153562	5	AC009046			AC009046 Homo sapi
c	9	20.4	85.0	168172	5	AC010528			AC010528 Homo sapi
	10	20.4	85.0	188557	15	AC106737			AC106737 Homo sapi
	11	20.4	85.0	253694	15	AC084005			AC084005 Homo sapi
	12	19.8	82.5	74459	5	BS000616			BS000616 Pan trogl
c	13	19.8	82.5	87804	15	AC139126			AC139126 Mus muscu
c	14	19.8	82.5	110000	14	CU207366_21			Continuation (22 o
c	15	19.8	82.5	150348	6	AC154699			AC154699 Mus muscu
c	16	19.8	82.5	169254	5	AC148934			AC148934 Pan trogl
c	17	19.8	82.5	173589	6	CT030695			CT030695 Mouse DNA
c	18	19.8	82.5	182377	6	AC127268			AC127268 Mus muscu
	19	19.8	82.5	191701	15	AC080189			AC080189 Homo sapi
	20	19.8	82.5	204742	16	AC172902			AC172902 Bos tauru
c	21	19.8	82.5	205053	5	AC011749			AC011749 Homo sapi
	22	19.8	82.5	214853	16	AC174691			AC174691 Bos tauru
	23	19.8	82.5	218340	15	AC110129			AC110129 Rattus no
	24	19.4	80.8	72137	5	AL356795			AL356795 Human DNA
	25	19.4	80.8	115866	5	AL627422			AL627422 Human DNA
c	26	19.4	80.8	177646	15	AC149257			AC149257 Papio anu
	27	19.4	80.8	184461	16	AC188978			AC188978 Zea mays
c	28	19.4	80.8	206089	16	CU407095			CU407095 Sus scrof
c	29	19.4	80.8	210940	16	AC197143			AC197143 Zea mays
c	30	19.2	80.0	620	7	BV307797			BV307797 S236P6201
c	31	19.2	80.0	630	4	AK250724			AK250724 Hordeum v
	32	19.2	80.0	1493	5	AK026202			AK026202 Homo sapi
	33	19.2	80.0	2970	2	CS033468			CS033468 Sequence
	34	19.2	80.0	2970	2	CS042420			CS042420 Sequence
	35	19.2	80.0	2970	5	BC040968			BC040968 Homo sapi
	36	19.2	80.0	3679	4	AB164319			AB164319 Bryopsis
	37	19.2	80.0	12944	5	DQ418808			DQ418808 Homo sapi
c	38	19.2	80.0	20230	4	AM449533			AM449533 Vitis vin
	39	19.2	80.0	52813	11	CU459123			CU459123 Zebrafish
c	40	19.2	80.0	76351	11	BX957329			BX957329 Zebrafish
	41	19.2	80.0	90139	16	AC174600			AC174600 Strongylo
	42	19.2	80.0	110000	4	AP008208_128			Continuation (129
c	43	19.2	80.0	110000	4	AP008210_182			Continuation (183
c	44	19.2	80.0	110000	14	CP000423_15			Continuation (16 o
	45	19.2	80.0	110000	14	AE017194_16			Continuation (17 o

ALIGNMENTS

RESULT 1

HUMDM DPR/c

LOCUS HUMDM DPR 1387 bp DNA linear PRI 07-NOV-1994

DEFINITION Human Duchenne muscular dystrophy gene, exon 1.

SCORE Search Results Details for Application 10539178 and Search Result 20080109_150539_us-10-539-178-2.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:12:07 ; Search time 1374 Seconds
(without alignments)
1429.452 Million cell updates/sec

Title: US-10-539-178-2
Perfect score: 24
Sequence: 1 tcatgtgttttagttctatcgcaaa 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_in:*
- 13: gb_om:*
- 14: gb_ba:*
- 15: gb_htgl:*

16: gb_htg2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	24	100.0	1387	5	HUMMDMPR	M32058 Human Duche
c	2	24	100.0	11747	5	AF276053S1	AF276053 Homo sapi
	3	24	100.0	133889	5	AL031643	AL031643 Human DNA
	4	24	100.0	185393	5	CR956355	CR956355 Pan trogl
c	5	20.8	86.7	29554	4	AM432735	AM432735 Vitis vin
c	6	20.4	85.0	206472	15	AC126091	AC126091 Rattus no
	7	19.4	80.8	171795	16	AC202651	AC202651 Nomascus
c	8	19.4	80.8	184786	5	AC198612	AC198612 Pongo pyg
	9	19.4	80.8	203832	5	AC198040	AC198040 Pongo pyg
	10	19.2	80.0	121639	16	AC177296	AC177296 Strongylo
c	11	19.2	80.0	160626	16	AC181464	AC181464 Strongylo
c	12	19.2	80.0	164119	16	CU329691	CU329691 Sus scrof
c	13	19.2	80.0	169464	16	AC180025	AC180025 Strongylo
c	14	19.2	80.0	170373	16	AC178677	AC178677 Strongylo
c	15	19.2	80.0	218427	6	AL645727	AL645727 Mouse DNA
	16	19.2	80.0	220992	16	AC180045	AC180045 Strongylo
	17	19.2	80.0	246025	16	AC202299	AC202299 Medicago
c	18	19.2	80.0	257850	16	AC163552	AC163552 Bos tauru
	19	18.8	78.3	110000	4	CR382139_02	Continuation (3 of
	20	18.8	78.3	110000	4	CR382139_03	Continuation (4 of
	21	18.8	78.3	153938	16	AC168572	AC168572 Strongylo
c	22	18.8	78.3	182110	15	AC027466	AC027466 Homo sapi
c	23	18.8	78.3	198687	5	AC093298	AC093298 Homo sapi
c	24	18.8	78.3	199133	11	BX323062	BX323062 Zebrafish
c	25	18.4	76.7	3016	4	AM473681	AM473681 Vitis vin
	26	18.4	76.7	3285	4	AM465910	AM465910 Vitis vin
c	27	18.4	76.7	68368	4	AM461419	AM461419 Vitis vin
c	28	18.4	76.7	165705	11	AL929074	AL929074 Zebrafish
	29	18.4	76.7	221953	15	AC130078	AC130078 Rattus no
	30	18.4	76.7	270120	15	AC128627	AC128627 Rattus no
c	31	18.2	75.8	1107	11	DQ018673	DQ018673 Plethodon
	32	18.2	75.8	3707	14	AF047839	AF047839 Pseudoalt
	33	18.2	75.8	6153	5	CR627432	CR627432 Homo sapi
	34	18.2	75.8	9894	11	AJ867256	AJ867256 Oncorhync
c	35	18.2	75.8	28538	15	AC023735	AC023735 Drosophil
c	36	18.2	75.8	35383	12	U41510	U41510 Caenorhabdi
c	37	18.2	75.8	71066	16	CT009626_3	Continuation (4 of
	38	18.2	75.8	101319	5	AL392109	AL392109 Human DNA
c	39	18.2	75.8	110000	16	CT009626_1	Continuation (2 of
c	40	18.2	75.8	134375	16	AC178147	AC178147 Strongylo
	41	18.2	75.8	138302	16	CU075371	CU075371 Sus scrof
	42	18.2	75.8	148101	16	AC199691	AC199691 Spermph
	43	18.2	75.8	149039	15	AC143506	AC143506 Macaca mu
c	44	18.2	75.8	151707	6	AC193858	AC193858 Mus muscu
c	45	18.2	75.8	155370	16	AC155783	AC155783 Papio anu

ALIGNMENTS

SCORE Search Results Details for Application 10539178 and Search Result 20080109_150548_us-10-539-178-1.rni.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:31:44 ; Search time 266 Seconds
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295.437 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5378416 seqs, 1963011933 residues

Total number of hits satisfying chosen parameters: 10756832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	16.8	84.0	453	7	US-09-925-065A-222523	Sequence 222523,
	5	16.8	84.0	453	7	US-09-925-065A-222524	Sequence 222524,
c	6	16.8	84.0	471	7	US-09-925-065A-569405	Sequence 569405,
c	7	16.8	84.0	476	7	US-09-925-065A-110478	Sequence 110478,
c	8	16.8	84.0	482	7	US-09-925-065A-817635	Sequence 817635,
c	9	16.8	84.0	487	7	US-09-925-065A-739090	Sequence 739090,
c	10	16.8	84.0	528	7	US-09-925-065A-906486	Sequence 906486,
c	11	16.8	84.0	533	7	US-09-925-065A-784229	Sequence 784229,
c	12	16.8	84.0	540	7	US-09-925-065A-180903	Sequence 180903,
c	13	16.8	84.0	540	7	US-09-925-065A-180904	Sequence 180904,
c	14	16.8	84.0	540	7	US-09-925-065A-180905	Sequence 180905,
c	15	16.8	84.0	574	7	US-09-925-065A-891843	Sequence 891843,
c	16	16.8	84.0	594	7	US-09-925-065A-311114	Sequence 311114,
c	17	16.8	84.0	599	7	US-09-925-065A-572287	Sequence 572287,
	18	16.8	84.0	602	7	US-09-925-065A-444385	Sequence 444385,
c	19	16.8	84.0	607	7	US-09-925-065A-530004	Sequence 530004,
	20	16.8	84.0	631	7	US-09-925-065A-395574	Sequence 395574,
	21	16.8	84.0	631	7	US-09-925-065A-395575	Sequence 395575,
c	22	16.8	84.0	631	7	US-09-925-065A-938412	Sequence 938412,
c	23	16.8	84.0	631	7	US-09-925-065A-938413	Sequence 938413,
	24	16.8	84.0	669	7	US-09-925-065A-907607	Sequence 907607,
c	25	16.8	84.0	670	7	US-09-925-065A-877462	Sequence 877462,
c	26	16.8	84.0	670	7	US-09-925-065A-906281	Sequence 906281,
	27	16.8	84.0	725	7	US-09-925-065A-717833	Sequence 717833,
	28	16.8	84.0	771	7	US-09-925-065A-939969	Sequence 939969,
	29	16.8	84.0	16922	3	US-09-949-002-671	Sequence 671, App
	30	16.8	84.0	16923	3	US-09-949-002-708	Sequence 708, App
c	31	16.4	82.0	449	7	US-09-925-065A-880454	Sequence 880454,
	32	16.4	82.0	455	7	US-09-925-065A-870559	Sequence 870559,
c	33	16.4	82.0	554	7	US-09-925-065A-201120	Sequence 201120,
	34	16.4	82.0	563	7	US-09-925-065A-190081	Sequence 190081,
c	35	16.4	82.0	568	7	US-09-925-065A-599747	Sequence 599747,
c	36	16.4	82.0	576	7	US-09-925-065A-415796	Sequence 415796,
c	37	16.4	82.0	601	3	US-09-949-016-96596	Sequence 96596, A
c	38	16.4	82.0	601	3	US-09-949-016-96597	Sequence 96597, A
c	39	16.4	82.0	601	3	US-09-949-016-96862	Sequence 96862, A
c	40	16.4	82.0	601	3	US-09-949-016-96863	Sequence 96863, A
c	41	16.4	82.0	601	3	US-09-949-016-97128	Sequence 97128, A
c	42	16.4	82.0	601	3	US-09-949-016-97129	Sequence 97129, A
c	43	16.4	82.0	601	3	US-09-949-016-97394	Sequence 97394, A
c	44	16.4	82.0	601	3	US-09-949-016-97395	Sequence 97395, A
c	45	16.4	82.0	601	3	US-09-949-016-97660	Sequence 97660, A

ALIGNMENTS

RESULT 1

US-09-949-016-12017/c

; Sequence 12017, Application US/09949016

; Patent No. 6812339

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295.437 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 10756832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 3	17.8	80.9	2956	7	US-09-925-065A-686159	Sequence 686159,
c 4	17.8	80.9	2956	7	US-09-925-065A-686160	Sequence 686160,
5	17.4	79.1	601	3	US-09-949-016-62517	Sequence 62517, A
c 6	17.4	79.1	163662	3	US-09-949-016-12545	Sequence 12545, A
c 7	17.4	79.1	163664	3	US-09-949-016-13546	Sequence 13546, A
8	17.2	78.2	561	7	US-09-925-065A-563013	Sequence 563013,
9	17.2	78.2	562	7	US-09-925-065A-395750	Sequence 395750,
10	17.2	78.2	594	5	US-10-703-032-81796	Sequence 81796, A
11	17.2	78.2	601	3	US-09-949-016-53876	Sequence 53876, A
c 12	17.2	78.2	614	7	US-09-925-065A-418559	Sequence 418559,
c 13	17.2	78.2	632	7	US-09-925-065A-93681	Sequence 93681, A
c 14	17.2	78.2	700	3	US-09-735-271-1113	Sequence 1113, Ap
15	17.2	78.2	2335	3	US-10-104-047-704	Sequence 704, App
16	17.2	78.2	75176	3	US-09-949-016-13300	Sequence 13300, A
c 17	17.2	78.2	187136	3	US-09-949-016-17231	Sequence 17231, A
18	17.2	78.2	360470	3	US-09-949-016-13173	Sequence 13173, A
c 19	16.8	76.4	547	7	US-09-925-065A-767437	Sequence 767437,
c 20	16.8	76.4	597	7	US-09-925-065A-748035	Sequence 748035,
c 21	16.8	76.4	608	7	US-09-925-065A-367436	Sequence 367436,
c 22	16.8	76.4	608	7	US-09-925-065A-786198	Sequence 786198,
c 23	16.8	76.4	608	7	US-09-925-065A-786199	Sequence 786199,
c 24	16.8	76.4	613	7	US-09-925-065A-833516	Sequence 833516,
c 25	16.8	76.4	617	7	US-09-925-065A-348908	Sequence 348908,
c 26	16.8	76.4	617	7	US-09-925-065A-348909	Sequence 348909,
c 27	16.8	76.4	634	7	US-09-925-065A-882797	Sequence 882797,
28	16.8	76.4	636	7	US-09-925-065A-356508	Sequence 356508,
29	16.8	76.4	636	7	US-09-925-065A-356509	Sequence 356509,
c 30	16.8	76.4	658	7	US-09-925-065A-806242	Sequence 806242,
c 31	16.8	76.4	659	7	US-09-925-065A-806236	Sequence 806236,
c 32	16.8	76.4	665	7	US-09-925-065A-748036	Sequence 748036,
c 33	16.8	76.4	667	7	US-09-925-065A-806740	Sequence 806740,
34	16.8	76.4	670	7	US-09-925-065A-765538	Sequence 765538,
35	16.8	76.4	726	7	US-09-925-065A-765539	Sequence 765539,
c 36	16.8	76.4	815	7	US-09-925-065A-7264	Sequence 7264, Ap
37	16.8	76.4	1431	7	US-09-925-065A-682858	Sequence 682858,
c 38	16.8	76.4	1743	6	US-11-601-793-7	Sequence 7, Appli
c 39	16.8	76.4	162025	3	US-09-834-700-13	Sequence 13, Appl
c 40	16.8	76.4	162025	3	US-09-834-700-14	Sequence 14, Appl
c 41	16.8	76.4	162025	3	US-09-834-700-17	Sequence 17, Appl
c 42	16.8	76.4	162025	3	US-09-834-700-18	Sequence 18, Appl
43	16.4	74.5	4267	3	US-09-023-655-1379	Sequence 1379, Ap
44	16.4	74.5	110243	3	US-09-949-016-13698	Sequence 13698, A
c 45	16.4	74.5	146428	3	US-09-949-016-12620	Sequence 12620, A

ALIGNMENTS

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; Sequence 914264, Application US/09925065A

; Patent No. H002191

; GENERAL INFORMATION:

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Listing first 45 summaries

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	7	19.2	80.0	538	7	US-09-925-065A-658760	Sequence 658760,
c	8	19.2	80.0	756	7	US-09-925-065A-686845	Sequence 686845,
c	9	18.4	76.7	695	7	US-09-925-065A-84644	Sequence 84644, A
c	10	18.4	76.7	1578	3	US-08-956-171E-216	Sequence 216, App
c	11	18.4	76.7	1578	3	US-08-781-986A-216	Sequence 216, App
	12	18.2	75.8	484	7	US-09-925-065A-104009	Sequence 104009,
	13	18.2	75.8	484	7	US-09-925-065A-104010	Sequence 104010,
	14	18.2	75.8	484	7	US-09-925-065A-104011	Sequence 104011,
	15	18.2	75.8	524	7	US-09-925-065A-620539	Sequence 620539,
	16	18.2	75.8	524	7	US-09-925-065A-620540	Sequence 620540,
	17	18.2	75.8	541	7	US-09-925-065A-369884	Sequence 369884,
	18	18.2	75.8	594	7	US-09-925-065A-950660	Sequence 950660,
c	19	18.2	75.8	601	3	US-09-949-016-141435	Sequence 141435,
	20	18.2	75.8	617	7	US-09-925-065A-863151	Sequence 863151,
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	22	18.2	75.8	1473	7	US-09-925-065A-715341	Sequence 715341,
	23	18.2	75.8	1473	7	US-09-925-065A-715342	Sequence 715342,
	24	18.2	75.8	236964	3	US-09-949-016-15753	Sequence 15753, A
	25	17.8	74.2	578	7	US-09-925-065A-618175	Sequence 618175,
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c	28	17.8	74.2	610	7	US-09-925-065A-772349	Sequence 772349,
c	29	17.8	74.2	644	7	US-09-925-065A-771937	Sequence 771937,
c	30	17.8	74.2	646	7	US-09-925-065A-836520	Sequence 836520,
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	34	17.8	74.2	11464	3	US-08-884-324-13	Sequence 13, Appl
	35	17.8	74.2	11464	3	US-09-479-862-13	Sequence 13, Appl
	36	17.8	74.2	11464	3	US-10-100-057-17	Sequence 17, Appl
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	40	17.8	74.2	28994	3	US-09-479-862-14	Sequence 14, Appl
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ALIGNMENTS

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US-09-949-016-189725

; Sequence 189725, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

SCORE Search Results Details for Application 10539178 Search Result 20080109_150548_us-10-539

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OM nucleic - nucleic search, using sw model

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(without alignments)
295.437 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 5378416 seqs, 1963011933 residues

Total number of hits satisfying chosen parameters: 10756832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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4	17.6	73.3	601	3	US-09-949-016-195566	Sequence 195566,
5	17.6	73.3	603	7	US-09-925-065A-362509	Sequence 362509,
6	17.6	73.3	603	7	US-09-925-065A-362510	Sequence 362510,
7	17.6	73.3	645	3	US-09-854-133-627	Sequence 627, App
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9	17.6	73.3	705	7	US-09-925-065A-921655	Sequence 921655,
10	17.6	73.3	1051	5	US-10-703-032-13950	Sequence 13950, A
c 11	17.6	73.3	1632	3	US-10-046-232-21	Sequence 21, Appl
c 12	17.6	73.3	1632	5	US-10-940-954-21	Sequence 21, Appl
c 13	17.6	73.3	2162	3	US-10-046-232-19	Sequence 19, Appl
c 14	17.6	73.3	2162	5	US-10-940-954-19	Sequence 19, Appl
15	17.6	73.3	3172	3	US-09-976-594-400	Sequence 400, App
16	17.6	73.3	3817	3	US-09-949-016-5552	Sequence 5552, Ap
17	17.6	73.3	3835	3	US-09-949-016-1067	Sequence 1067, Ap
18	17.6	73.3	27236	3	US-09-949-016-12809	Sequence 12809, A
19	17.6	73.3	27241	3	US-09-949-016-17294	Sequence 17294, A
20	17.4	72.5	2172	4	US-10-154-419-9	Sequence 9, Appli
21	17.4	72.5	2634	4	US-10-154-419-7	Sequence 7, Appli
c 22	17.2	71.7	599	7	US-09-925-065A-342808	Sequence 342808,
c 23	17.2	71.7	599	7	US-09-925-065A-342809	Sequence 342809,
24	17.2	71.7	603	7	US-09-925-065A-640091	Sequence 640091,
c 25	17.2	71.7	617	7	US-09-925-065A-761196	Sequence 761196,
c 26	17.2	71.7	618	7	US-09-925-065A-754837	Sequence 754837,
c 27	17.2	71.7	629	7	US-09-925-065A-255332	Sequence 255332,
c 28	17.2	71.7	629	7	US-09-925-065A-255333	Sequence 255333,
29	17.2	71.7	9143	5	US-09-619-049-173	Sequence 173, App
30	17.2	71.7	15051	5	US-09-619-049-172	Sequence 172, App
31	17	70.8	24221	3	US-09-949-016-14964	Sequence 14964, A
32	16.8	70.0	513	7	US-09-925-065A-625641	Sequence 625641,
c 33	16.8	70.0	606	7	US-09-925-065A-314732	Sequence 314732,
c 34	16.8	70.0	632	7	US-09-925-065A-793171	Sequence 793171,
c 35	16.8	70.0	651	7	US-09-925-065A-788332	Sequence 788332,
c 36	16.8	70.0	651	7	US-09-925-065A-846702	Sequence 846702,
c 37	16.8	70.0	651	7	US-09-925-065A-846703	Sequence 846703,
c 38	16.8	70.0	232024	3	US-09-949-016-13477	Sequence 13477, A
c 39	16.6	69.2	24	6	US-10-310-914B-840272	Sequence 840272,
40	16.6	69.2	555	7	US-09-925-065A-164065	Sequence 164065,
41	16.6	69.2	555	7	US-09-925-065A-164066	Sequence 164066,
c 42	16.6	69.2	582	7	US-09-925-065A-271253	Sequence 271253,
c 43	16.6	69.2	582	7	US-09-925-065A-271254	Sequence 271254,
c 44	16.6	69.2	602	7	US-09-925-065A-147917	Sequence 147917,
c 45	16.6	69.2	602	7	US-09-925-065A-147918	Sequence 147918,

ALIGNMENTS

RESULT 1

US-09-949-016-16515/c

; Sequence 16515, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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(without alignments)
233.030 Million cell updates/sec

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Perfect score: 20
Sequence: 1 aattggcaccagagaaatgg 20

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	18.4	92.0	377	13	US-10-301-480-615568	Sequence 615568,
c	5	18.4	92.0	397	26	US-11-497-489A-9885	Sequence 9885, Ap
c	6	18.4	92.0	430	13	US-10-301-480-2271	Sequence 2271, Ap
c	7	18.4	92.0	430	13	US-10-301-480-615680	Sequence 615680,
c	8	18.4	92.0	478	26	US-11-497-489A-236963	Sequence 236963,
c	9	18.4	92.0	886	7	US-10-027-632-2657	Sequence 2657, Ap
c	10	18.4	92.0	886	8	US-10-027-632-2657	Sequence 2657, Ap
	11	18.4	92.0	956	13	US-10-301-480-533405	Sequence 533405,
	12	18.4	92.0	956	13	US-10-301-480-1146814	Sequence 1146814,
c	13	18.4	92.0	85869	16	US-10-940-774-12017	Sequence 12017, A
c	14	18.4	92.0	85878	16	US-10-940-774-16321	Sequence 16321, A
c	15	17.4	87.0	315	26	US-11-497-489A-139971	Sequence 139971,
c	16	17.4	87.0	444	26	US-11-497-489A-168595	Sequence 168595,
c	17	17.4	87.0	471	26	US-11-497-489A-168427	Sequence 168427,
c	18	17.4	87.0	611	4	US-09-925-065A-626421	Sequence 626421,
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c	23	17	85.0	1188	11	US-10-750-623-64683	Sequence 64683, A
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	28	16.8	84.0	201	15	US-10-767-471-23710	Sequence 23710, A
	29	16.8	84.0	201	15	US-10-767-471-23713	Sequence 23713, A
	30	16.8	84.0	201	16	US-10-990-328-237300	Sequence 237300,
	31	16.8	84.0	201	16	US-10-990-328-237301	Sequence 237301,
c	32	16.8	84.0	231	26	US-11-497-489A-150660	Sequence 150660,
c	33	16.8	84.0	249	26	US-11-497-489A-45367	Sequence 45367, A
c	34	16.8	84.0	277	26	US-11-497-489A-123526	Sequence 123526,
c	35	16.8	84.0	290	26	US-11-497-489A-7563	Sequence 7563, Ap
	36	16.8	84.0	293	23	US-11-521-349-10419	Sequence 10419, A
	37	16.8	84.0	293	25	US-11-503-243A-431334	Sequence 431334,

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Maximum Match 100%
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c 4	18.8	85.5	691	5	US-09-925-065A-914264	Sequence 914264,
5	18.4	83.6	201	16	US-10-990-328-171628	Sequence 171628,
c 6	18.4	83.6	523	4	US-09-925-065A-457123	Sequence 457123,
c 7	18.4	83.6	523	5	US-09-925-065A-457123	Sequence 457123,
c 8	18.4	83.6	540	13	US-10-301-480-515054	Sequence 515054,
c 9	18.4	83.6	540	13	US-10-301-480-1128463	Sequence 1128463,
10	18.4	83.6	139110	16	US-10-990-328-94076	Sequence 94076, A
11	17.8	80.9	25	29	US-11-695-599-222923	Sequence 222923,
12	17.8	80.9	25	29	US-11-695-599-467600	Sequence 467600,
c 13	17.8	80.9	33	24	US-11-406-880B-23795	Sequence 23795, A
c 14	17.8	80.9	472	10	US-10-425-115-173837	Sequence 173837,
c 15	17.8	80.9	700	26	US-11-443-428A-229378	Sequence 229378,
c 16	17.8	80.9	1510	11	US-10-487-901-3616	Sequence 3616, Ap
c 17	17.8	80.9	1510	11	US-10-487-901-7291	Sequence 7291, Ap
18	17.8	80.9	2805	9	US-10-424-599-47506	Sequence 47506, A
c 19	17.8	80.9	2956	4	US-09-925-065A-686159	Sequence 686159,
c 20	17.8	80.9	2956	4	US-09-925-065A-686160	Sequence 686160,
c 21	17.8	80.9	2956	5	US-09-925-065A-686159	Sequence 686159,
c 22	17.8	80.9	2956	5	US-09-925-065A-686160	Sequence 686160,
23	17.4	79.1	601	16	US-10-940-774-62517	Sequence 62517, A
c 24	17.4	79.1	163662	16	US-10-940-774-12545	Sequence 12545, A
c 25	17.4	79.1	163664	16	US-10-940-774-13546	Sequence 13546, A
c 26	17.2	78.2	368	25	US-11-486-448-29255	Sequence 29255, A
c 27	17.2	78.2	368	25	US-11-503-243A-238507	Sequence 238507,
c 28	17.2	78.2	490	27	US-11-486-299A-28528	Sequence 28528, A
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SUMMARIES

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4	22.4	93.3	197131	16	US-10-940-774-12675	Sequence 12675, A
5	22.4	93.3	197132	16	US-10-940-774-17170	Sequence 17170, A
6	22.4	93.3	209822	10	US-10-741-600-17560	Sequence 17560, A
7	22.4	93.3	209822	11	US-10-995-561-13198	Sequence 13198, A
8	22.4	93.3	209822	15	US-10-796-280-12169	Sequence 12169, A
9	20.4	85.0	523	4	US-09-925-065A-24021	Sequence 24021, A
10	20.4	85.0	523	5	US-09-925-065A-24021	Sequence 24021, A
11	20.4	85.0	523	13	US-10-301-480-125258	Sequence 125258,
12	20.4	85.0	523	13	US-10-301-480-738667	Sequence 738667,
13	19.4	80.8	426	29	US-11-239-625A-1152	Sequence 1152, Ap
14	19.4	80.8	437	29	US-11-239-625A-1155	Sequence 1155, Ap
c 15	19.4	80.8	568	4	US-09-925-065A-237168	Sequence 237168,
c 16	19.4	80.8	568	5	US-09-925-065A-237168	Sequence 237168,
c 17	19.4	80.8	641	26	US-11-443-428A-467880	Sequence 467880,
18	19.2	80.0	32	17	US-10-535-164-277476	Sequence 277476,
19	19.2	80.0	64	25	US-11-130-645A-429715	Sequence 429715,
c 20	19.2	80.0	464	4	US-09-925-065A-810864	Sequence 810864,
c 21	19.2	80.0	464	5	US-09-925-065A-810864	Sequence 810864,
22	19.2	80.0	538	4	US-09-925-065A-658760	Sequence 658760,
23	19.2	80.0	538	5	US-09-925-065A-658760	Sequence 658760,
24	19.2	80.0	600	11	US-10-972-079-83593	Sequence 83593, A
25	19.2	80.0	600	11	US-10-972-079-83594	Sequence 83594, A
26	19.2	80.0	600	11	US-10-972-079-83595	Sequence 83595, A
c 27	19.2	80.0	756	4	US-09-925-065A-686845	Sequence 686845,
c 28	19.2	80.0	756	5	US-09-925-065A-686845	Sequence 686845,
29	19.2	80.0	1000	21	US-11-266-748A-283981	Sequence 283981,
c 30	19.2	80.0	1000	21	US-11-266-748A-335410	Sequence 335410,
31	19.2	80.0	1000	21	US-11-266-748A-393829	Sequence 393829,
c 32	19.2	80.0	1000	21	US-11-266-748A-464875	Sequence 464875,
33	19.2	80.0	1438	26	US-11-443-428A-730445	Sequence 730445,
34	19.2	80.0	1501	6	US-09-815-264-51827	Sequence 51827, A
35	19.2	80.0	1501	27	US-11-595-983-51827	Sequence 51827, A
36	19.2	80.0	2218	26	US-11-443-428A-460989	Sequence 460989,
37	19.2	80.0	2942	25	US-11-433-832-44604	Sequence 44604, A

SCORE Search Results Details for Application 10539178 and Search Result 20080109_150553_us-10-539-178-2.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:35:15 ; Search time 2572 Seconds
(without alignments)
233.030 Million cell updates/sec

Title: US-10-539-178-2
Perfect score: 24
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34378780 seqs, 12487843900 residues

Total number of hits satisfying chosen parameters: 68757560

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /ABSS/Data/CRF/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /ABSS/Data/CRF/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /ABSS/Data/CRF/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /ABSS/Data/CRF/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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- 6: /ABSS/Data/CRF/ptodata/2/pubpna/US09D_PUBCOMB.seq:*
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- 13: /ABSS/Data/CRF/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
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 24: /ABSS/Data/CRF/ptodata/2/pubpna/US11G_PUBCOMB.seq:*
 25: /ABSS/Data/CRF/ptodata/2/pubpna/US11H_PUBCOMB.seq:*
 26: /ABSS/Data/CRF/ptodata/2/pubpna/US11I_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	100.0	24	14	US-10-539-178-2	Sequence 2, Appli
c 2	18.2	75.8	302	26	US-11-497-489A-250518	Sequence 250518,
c 3	18.2	75.8	372	26	US-11-497-489A-242942	Sequence 242942,
c 4	18.2	75.8	391	26	US-11-497-489A-142573	Sequence 142573,
c 5	18.2	75.8	393	26	US-11-497-489A-170489	Sequence 170489,
c 6	18.2	75.8	439	26	US-11-497-489A-72756	Sequence 72756, A
c 7	18.2	75.8	624	26	US-11-497-489A-41562	Sequence 41562, A
c 8	18.2	75.8	1039	9	US-10-424-599-90058	Sequence 90058, A
c 9	18.2	75.8	131780	16	US-10-990-328-97256	Sequence 97256, A
c 10	18.2	75.8	163022	16	US-10-940-774-16515	Sequence 16515, A
11	18.2	75.8	191410	16	US-10-990-328-95165	Sequence 95165, A
12	18.2	75.8	221600	11	US-10-840-590-1	Sequence 1, Appli
13	17.8	74.2	1147	23	US-11-491-125A-62465	Sequence 62465, A
14	17.8	74.2	7519	23	US-11-491-125A-50542	Sequence 50542, A
15	17.8	74.2	19332	23	US-11-491-125A-8715	Sequence 8715, Ap
c 16	17.8	74.2	38068	23	US-11-491-125A-16861	Sequence 16861, A
17	17.8	74.2	51472	6	US-09-815-264-81524	Sequence 81524, A
18	17.8	74.2	51472	27	US-11-595-983-81524	Sequence 81524, A
c 19	17.8	74.2	118315	6	US-09-815-264-70214	Sequence 70214, A
c 20	17.8	74.2	118315	27	US-11-595-983-70214	Sequence 70214, A
21	17.6	73.3	64	23	US-11-511-035-448361	Sequence 448361,
22	17.6	73.3	201	16	US-10-990-328-453999	Sequence 453999,
23	17.6	73.3	380	9	US-10-242-535A-16641	Sequence 16641, A
24	17.6	73.3	380	9	US-10-085-783A-16641	Sequence 16641, A
c 25	17.6	73.3	383	27	US-11-486-299A-57799	Sequence 57799, A
26	17.6	73.3	387	26	US-11-497-489A-46515	Sequence 46515, A
27	17.6	73.3	399	3	US-09-918-995-36182	Sequence 36182, A
c 28	17.6	73.3	417	26	US-11-497-489A-185338	Sequence 185338,
c 29	17.6	73.3	443	26	US-11-497-489A-45750	Sequence 45750, A
30	17.6	73.3	507	7	US-10-102-524-1373	Sequence 1373, Ap
31	17.6	73.3	557	26	US-11-443-428A-85105	Sequence 85105, A
32	17.6	73.3	567	4	US-09-925-065A-57825	Sequence 57825, A
33	17.6	73.3	567	5	US-09-925-065A-57825	Sequence 57825, A
34	17.6	73.3	567	13	US-10-301-480-159063	Sequence 159063,
35	17.6	73.3	567	13	US-10-301-480-772472	Sequence 772472,
36	17.6	73.3	600	14	US-10-956-160-215646	Sequence 215646,
37	17.6	73.3	601	14	US-10-956-160-5539	Sequence 5539, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2008, 19:38:20 ; Search time 4 Seconds
(without alignments)
18.095 Million cell updates/sec

Title: US-10-539-178-1
Perfect score: 20
Sequence: 1 aattggcaccagagaaatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5859 seqs, 2010571 residues

Total number of hits satisfying chosen parameters: 11718

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /ABSS/Data/CRF/ptodata/1/pubpna/US10_NEW_PUB.seq:*
2: /ABSS/Data/CRF/ptodata/1/pubpna/US11_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	1	12.8	64.0	439	1 US-10-959-789-508	Sequence 508, App
c	2	12.8	64.0	762	2 US-11-781-818-63	Sequence 63, Appl
c	3	12.8	64.0	762	2 US-11-781-818-64	Sequence 64, Appl

c	4	12.8	64.0	1242	2	US-11-558-961-5	Sequence 5, Appli
	5	12.6	63.0	277	1	US-10-959-789-2568	Sequence 2568, Ap
c	6	12.6	63.0	1962	2	US-11-801-040-24	Sequence 24, Appl
	7	12.6	63.0	2421	1	US-10-598-073-19	Sequence 19, Appl
	8	12.6	63.0	6016	2	US-11-676-172-3	Sequence 3, Appli
	9	12.6	63.0	9941	2	US-11-683-962-3	Sequence 3, Appli
	10	12.6	63.0	9941	2	US-11-689-407-3	Sequence 3, Appli
	11	12.4	62.0	523	1	US-10-959-789-2687	Sequence 2687, Ap
	12	12.2	61.0	312	1	US-10-959-789-2726	Sequence 2726, Ap
c	13	12.2	61.0	997	2	US-11-801-040-33	Sequence 33, Appl
c	14	12.2	61.0	1568	2	US-11-220-398A-69	Sequence 69, Appl
c	15	12.2	61.0	2128	2	US-11-220-398A-22	Sequence 22, Appl
c	16	12	60.0	71	2	US-11-753-263-78	Sequence 78, Appl
c	17	12	60.0	131	2	US-11-676-985-2	Sequence 2, Appli
c	18	11.8	59.0	96	1	US-10-959-789-909	Sequence 909, App
c	19	11.8	59.0	226	1	US-10-959-789-927	Sequence 927, App
c	20	11.8	59.0	228	1	US-10-959-789-928	Sequence 928, App
c	21	11.8	59.0	263	1	US-10-959-789-924	Sequence 924, App
c	22	11.8	59.0	266	1	US-10-959-789-923	Sequence 923, App
c	23	11.8	59.0	271	1	US-10-959-789-922	Sequence 922, App
c	24	11.8	59.0	293	1	US-10-959-789-2632	Sequence 2632, Ap
c	25	11.8	59.0	300	1	US-10-959-789-921	Sequence 921, App
c	26	11.8	59.0	303	1	US-10-959-789-862	Sequence 862, App
c	27	11.8	59.0	316	1	US-10-959-789-920	Sequence 920, App
	28	11.8	59.0	5289	2	US-11-220-398A-212	Sequence 212, App
c	29	11.6	58.0	67	2	US-11-753-263-52	Sequence 52, Appl
	30	11.6	58.0	221	1	US-10-959-789-758	Sequence 758, App
	31	11.6	58.0	299	1	US-10-959-789-933	Sequence 933, App
c	32	11.6	58.0	489	1	US-10-959-789-930	Sequence 930, App
c	33	11.6	58.0	519	1	US-10-959-789-849	Sequence 849, App
	34	11.6	58.0	1228	2	US-11-801-040-25	Sequence 25, Appl
	35	11.6	58.0	2369	2	US-11-823-707-1	Sequence 1, Appli
	36	11.6	58.0	2369	2	US-11-823-707-2	Sequence 2, Appli
c	37	11.6	58.0	2391	1	US-10-598-073-25	Sequence 25, Appl
c	38	11.6	58.0	6177	2	US-11-668-333-44	Sequence 44, Appl
	39	11.4	57.0	287	1	US-10-959-789-2750	Sequence 2750, Ap
	40	11.4	57.0	298	1	US-10-959-789-2787	Sequence 2787, Ap
c	41	11.4	57.0	571	1	US-10-959-789-464	Sequence 464, App
	42	11.4	57.0	1379	2	US-11-801-040-18	Sequence 18, Appl
c	43	11.4	57.0	6127	2	US-11-401-765-1	Sequence 1, Appli
c	44	11.2	56.0	70	2	US-11-753-263-79	Sequence 79, Appl
c	45	11.2	56.0	70	2	US-11-753-263-241	Sequence 241, App

ALIGNMENTS

RESULT 1

US-10-959-789-508/c

; Sequence 508, Application US/10959789

; Publication No. US20080005809A1

; GENERAL INFORMATION:

; APPLICANT: Bledig, Stefan A.

; APPLICANT: Byrum, Joseph R.

; APPLICANT: Liu, Jingdong

; TITLE OF INVENTION: Nucleic Acid molecules And Other Molecules Associated With The

; TITLE OF INVENTION: Methionine Synthesis And Degradation Pathways

; FILE REFERENCE: 16517.328

; CURRENT APPLICATION NUMBER: US/10/959,789

; CURRENT FILING DATE: 2004-10-07

; PRIOR APPLICATION NUMBER: US 09/198,779

c	4	12.6	57.3	1410	2	US-11-495-624-626	Sequence 626, App
c	5	12.6	57.3	1410	2	US-11-495-624-627	Sequence 627, App
	6	12.6	57.3	8730	2	US-11-668-333-43	Sequence 43, Appl
c	7	12.4	56.4	1953	2	US-11-220-398A-112	Sequence 112, App
c	8	12.4	56.4	2175	2	US-11-220-398A-110	Sequence 110, App
c	9	12.4	56.4	2316	2	US-11-220-398A-116	Sequence 116, App
c	10	12.4	56.4	2538	2	US-11-220-398A-114	Sequence 114, App
c	11	12.4	56.4	3168	2	US-11-684-979-23	Sequence 23, Appl
c	12	12.4	56.4	4854	2	US-11-220-398A-118	Sequence 118, App
c	13	12.4	56.4	5076	2	US-11-220-398A-104	Sequence 104, App
c	14	12.4	56.4	8578	2	US-11-220-398A-120	Sequence 120, App
c	15	12.2	55.5	317	1	US-10-959-789-2425	Sequence 2425, Ap
	16	12.2	55.5	1730	2	US-11-558-961-7	Sequence 7, Appli
c	17	12.2	55.5	3730	2	US-11-713-291-8	Sequence 8, Appli
c	18	12.2	55.5	7934	2	US-11-713-291-1	Sequence 1, Appli
	19	12	54.5	180	1	US-10-959-789-2261	Sequence 2261, Ap
	20	12	54.5	257	1	US-10-959-789-2601	Sequence 2601, Ap
	21	12	54.5	269	1	US-10-959-789-2593	Sequence 2593, Ap
	22	12	54.5	274	1	US-10-959-789-2600	Sequence 2600, Ap
	23	12	54.5	274	1	US-10-959-789-2613	Sequence 2613, Ap
	24	12	54.5	292	1	US-10-959-789-2583	Sequence 2583, Ap
	25	12	54.5	294	1	US-10-959-789-2552	Sequence 2552, Ap
	26	12	54.5	297	1	US-10-959-789-2541	Sequence 2541, Ap
	27	12	54.5	298	1	US-10-959-789-2553	Sequence 2553, Ap
	28	12	54.5	298	1	US-10-959-789-2591	Sequence 2591, Ap
	29	12	54.5	306	1	US-10-959-789-2581	Sequence 2581, Ap
	30	12	54.5	326	1	US-10-959-789-2533	Sequence 2533, Ap
	31	12	54.5	343	1	US-10-959-789-2548	Sequence 2548, Ap
	32	12	54.5	476	1	US-10-959-789-2486	Sequence 2486, Ap
	33	12	54.5	504	1	US-10-959-789-2492	Sequence 2492, Ap
c	34	12	54.5	1914	2	US-11-801-040-34	Sequence 34, Appl
c	35	11.8	53.6	1692	2	US-11-676-172-9	Sequence 9, Appli
	36	11.8	53.6	6177	2	US-11-668-333-44	Sequence 44, Appl
c	37	11.6	52.7	189	1	US-10-564-615-44	Sequence 44, Appl
	38	11.6	52.7	243	1	US-10-959-789-866	Sequence 866, App
	39	11.6	52.7	249	1	US-10-959-789-344	Sequence 344, App
	40	11.6	52.7	292	1	US-10-959-789-870	Sequence 870, App
c	41	11.6	52.7	799	2	US-11-835-872-1	Sequence 1, Appli
c	42	11.6	52.7	2391	1	US-10-598-073-25	Sequence 25, Appl
c	43	11.6	52.7	5279	1	US-10-592-066-1	Sequence 1, Appli
	44	11.6	52.7	6127	2	US-11-401-765-1	Sequence 1, Appli
	45	11.6	52.7	7934	2	US-11-713-291-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-11-617-282-11/c

; Sequence 11, Application US/11617282

; Publication No. US20080003596A1

; GENERAL INFORMATION:

; APPLICANT: AKAHOSHI, EIICHI

; APPLICANT: YOSHIMURA, SEIKO

; APPLICANT: ISHIHARA, MITSUKO

; TITLE OF INVENTION: VECTOR AND METHOD FOR DETECTING THE CHANGE IN TRANSCRIPTION AMC

; FILE REFERENCE: 301374US

; CURRENT APPLICATION NUMBER: US/11/617,282

; CURRENT FILING DATE: 2006-12-28

; PRIOR APPLICATION NUMBER: JP 2006-000135

; PRIOR FILING DATE: 2006-01-04

**SCORE Search Results Details for Application
10539178 and Search Result
20080109_150558_us-10-539-178-188.rnpbn.**

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

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Run on:      January  9, 2008, 19:38:20 ; Search time 5 Seconds
              (without alignments)
              18.095 Million cell updates/sec
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Title: US-10-539-178-188
Perfect score: 24
Sequence: 1 tttatgcttctttgcaaactactg 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5859 seqs, 2010571 residues

Total number of hits satisfying chosen parameters: 11718

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :      Published_Applications_NA_New:*
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2:   /ABSS/Data/CRF/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	15.6	65.0	6085	2	US-11-676-172-1	Sequence 1, Appli
	2	14.4	60.0	1390	2	US-11-801-040-20	Sequence 20, Appl
c	3	14.2	59.2	1164	2	US-11-739-739-11	Sequence 11, Appl

c	4	13.8	57.5	1242	2	US-11-558-961-5	Sequence 5, Appli
	5	13.6	56.7	8730	2	US-11-668-333-43	Sequence 43, Appl
	6	13.4	55.8	122	1	US-10-564-615-93	Sequence 93, Appl
c	7	13.2	55.0	5925	2	US-11-676-172-5	Sequence 5, Appli
c	8	13.2	55.0	6016	2	US-11-676-172-3	Sequence 3, Appli
	9	13	54.2	173	1	US-10-564-615-63	Sequence 63, Appl
c	10	13	54.2	334	1	US-10-959-789-2997	Sequence 2997, Ap
c	11	13	54.2	603	1	US-10-594-298-1	Sequence 1, Appli
c	12	13	54.2	2590	2	US-11-781-818-85	Sequence 85, Appl
	13	12.8	53.3	1076	2	US-11-801-040-17	Sequence 17, Appl
c	14	12.8	53.3	4854	2	US-11-220-398A-118	Sequence 118, App
c	15	12.8	53.3	5076	2	US-11-220-398A-104	Sequence 104, App
	16	12.8	53.3	6177	2	US-11-668-333-44	Sequence 44, Appl
c	17	12.8	53.3	8578	2	US-11-220-398A-120	Sequence 120, App
c	18	12.6	52.5	2017	2	US-11-801-040-45	Sequence 45, Appl
c	19	12.6	52.5	2026	2	US-11-801-040-30	Sequence 30, Appl
c	20	12.6	52.5	3048	2	US-11-684-979-13	Sequence 13, Appl
c	21	12.6	52.5	3114	2	US-11-684-979-11	Sequence 11, Appl
c	22	12.6	52.5	3730	2	US-11-713-291-8	Sequence 8, Appli
c	23	12.6	52.5	7934	2	US-11-713-291-1	Sequence 1, Appli
	24	12.4	51.7	214	1	US-10-564-615-34	Sequence 34, Appl
c	25	12.4	51.7	2139	2	US-11-684-979-15	Sequence 15, Appl
c	26	12.2	50.8	165	2	US-11-617-282-7	Sequence 7, Appli
c	27	12.2	50.8	1264	2	US-11-801-040-32	Sequence 32, Appl
c	28	12.2	50.8	1542	1	US-10-590-661-8	Sequence 8, Appli
c	29	12.2	50.8	1542	1	US-10-590-661-10	Sequence 10, Appl
	30	12.2	50.8	3208	2	US-11-220-398A-103	Sequence 103, App
c	31	12.2	50.8	8730	2	US-11-668-333-43	Sequence 43, Appl
c	32	12.2	50.8	9941	2	US-11-683-962-3	Sequence 3, Appli
c	33	12.2	50.8	9941	2	US-11-689-407-3	Sequence 3, Appli
	34	12	50.0	306	1	US-10-959-789-2484	Sequence 2484, Ap
c	35	12	50.0	499	1	US-10-959-789-2665	Sequence 2665, Ap
c	36	12	50.0	811	2	US-11-791-839-6	Sequence 6, Appli
c	37	12	50.0	1169	2	US-11-801-040-11	Sequence 11, Appl
	38	12	50.0	1340	2	US-11-801-040-26	Sequence 26, Appl
c	39	12	50.0	2247	2	US-11-220-398A-37	Sequence 37, Appl
	40	12	50.0	8578	2	US-11-220-398A-120	Sequence 120, App
	41	11.8	49.2	270	1	US-10-959-789-893	Sequence 893, App
	42	11.8	49.2	282	1	US-10-959-789-892	Sequence 892, App
c	43	11.8	49.2	295	1	US-10-959-789-804	Sequence 804, App
	44	11.8	49.2	442	1	US-10-959-789-737	Sequence 737, App
	45	11.8	49.2	489	1	US-10-959-789-2797	Sequence 2797, Ap

ALIGNMENTS

RESULT 1

US-11-676-172-1/c

; Sequence 1, Application US/11676172

; Publication No. US20080004713A1

; GENERAL INFORMATION:

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; TITLE OF INVENTION: SCAFFOLD-FREE SELF-ORGANIZED 3D SYNTHETIC TISSUE

; FILE REFERENCE: 690128.401C1

SCORE Search Results Details for Application 10539178 and Search Result 20080109_150558_us-10-539-178-2.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10539178 and Search Result 20080109_150558_us-10-539-178-2.rnpbn.

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OM nucleic - nucleic search, using sw model

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Run on:      January  9, 2008, 19:38:20 ; Search time 5 Seconds
              (without alignments)
              18.095 Million cell updates/sec
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1 Title:          US-10-539-178-2
  Perfect score:  24
  Sequence:       1 tcatgtgttttagttctatcgc aaa 24

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5859 seqs, 2010571 residues

Total number of hits satisfying chosen parameters: 11718

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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1:   /ABSS/Data/CRF/ptodata/1/pubpna/US10_NEW_PUB.seq:*
2:   /ABSS/Data/CRF/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15.4	64.2	758	2	US-11-617-282-8	Sequence 8, Appli
2	15.4	64.2	1836	2	US-11-617-282-9	Sequence 9, Appli
3	14.6	60.8	1708	2	US-11-495-624-628	Sequence 628, App

	4	14.6	60.8	1708	2	US-11-495-624-629	Sequence 629, App
	5	14.6	60.8	1833	2	US-11-670-902-35	Sequence 35, Appl
	6	14.6	60.8	1836	2	US-11-670-902-13	Sequence 13, Appl
	7	14.6	60.8	1851	2	US-11-670-902-21	Sequence 21, Appl
	8	14.6	60.8	1857	2	US-11-670-902-23	Sequence 23, Appl
	9	14.6	60.8	1862	2	US-11-670-902-27	Sequence 27, Appl
	10	14.6	60.8	1865	2	US-11-670-902-25	Sequence 25, Appl
	11	14.6	60.8	1878	2	US-11-670-902-5	Sequence 5, Appli
	12	14.6	60.8	1884	2	US-11-670-902-19	Sequence 19, Appl
	13	13.4	55.8	1310	2	US-11-801-040-12	Sequence 12, Appl
	14	13	54.2	1707	2	US-11-670-902-33	Sequence 33, Appl
	15	13	54.2	2428	2	US-11-572-719-19	Sequence 19, Appl
c	16	12.6	52.5	6177	2	US-11-668-333-44	Sequence 44, Appl
	17	12.4	51.7	287	1	US-10-959-789-905	Sequence 905, App
	18	12.4	51.7	1205	1	US-10-590-886-1	Sequence 1, Appli
c	19	12.4	51.7	1836	2	US-11-617-282-9	Sequence 9, Appli
	20	12.4	51.7	2139	2	US-11-684-979-15	Sequence 15, Appl
c	21	12.4	51.7	2274	2	US-11-220-398A-60	Sequence 60, Appl
c	22	12.4	51.7	2727	2	US-11-220-398A-38	Sequence 38, Appl
c	23	12.4	51.7	2961	2	US-11-684-979-9	Sequence 9, Appli
c	24	12.4	51.7	3160	2	US-11-220-398A-62	Sequence 62, Appl
c	25	12.2	50.8	114	2	US-11-495-624-149	Sequence 149, App
c	26	12.2	50.8	114	2	US-11-495-624-150	Sequence 150, App
c	27	12.2	50.8	317	1	US-10-959-789-1645	Sequence 1645, Ap
	28	12	50.0	292	1	US-10-959-789-627	Sequence 627, App
	29	12	50.0	334	1	US-10-959-789-2648	Sequence 2648, Ap
	30	12	50.0	340	1	US-10-959-789-580	Sequence 580, App
	31	12	50.0	6834	2	US-11-849-643-5	Sequence 5, Appli
	32	11.8	49.2	137	1	US-10-564-615-40	Sequence 40, Appl
c	33	11.8	49.2	144	1	US-10-564-615-71	Sequence 71, Appl
	34	11.8	49.2	277	1	US-10-959-789-943	Sequence 943, App
c	35	11.8	49.2	310	1	US-10-959-789-898	Sequence 898, App
c	36	11.8	49.2	454	1	US-10-959-789-897	Sequence 897, App
c	37	11.8	49.2	1431	2	US-11-801-040-21	Sequence 21, Appl
	38	11.8	49.2	1962	2	US-11-801-040-24	Sequence 24, Appl
c	39	11.8	49.2	2476	2	US-11-792-242-6	Sequence 6, Appli
	40	11.8	49.2	3712	2	US-11-684-979-61	Sequence 61, Appl
	41	11.6	48.3	602	1	US-10-959-789-1044	Sequence 1044, Ap
	42	11.6	48.3	2391	1	US-10-598-073-25	Sequence 25, Appl
c	43	11.4	47.5	67	2	US-11-753-263-334	Sequence 334, App
c	44	11.4	47.5	70	2	US-11-753-263-158	Sequence 158, App
c	45	11.4	47.5	103	1	US-10-564-615-124	Sequence 124, App

ALIGNMENTS

RESULT 1

US-11-617-282-8

; Sequence 8, Application US/11617282

; Publication No. US20080003596A1

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; TITLE OF INVENTION: VECTOR AND METHOD FOR DETECTING THE CHANGE IN TRANSCRIPTION AMC

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